AMENDMENTS TO THE CLAIMS

This listing replaces all prior versions and listings of claims in the application.

Listing of Claims

1. – 3.   (Canceled).

3.   (Withdrawn) An information recording medium in which program information for causing a computer system to carry out the individual procedures making up said biopolymer automatic identifying method according to claim 1 or 2 is stored.

4.   (New) A biopolymer automatic identifying method, comprising:

(a) providing a plurality of mass values obtained by subjecting a sample comprised of one or more biopolymers to MS/MS;

(b) matching at least one of said mass values with a theoretical mass of at least one candidate molecule in a predetermined database; then,

(c) in the event that multiple candidate molecules are matched in (b), selecting at least one candidate molecule from (b) that has a high similarity score;

(d) calibrating the obtained plurality of mass values from (a) using, as an internal reference:

(i) the theoretical mass of the candidate molecule in (b), in the event of only one matched candidate molecule, or

(ii) the theoretical mass of the selected candidate molecule or molecules in (c), in the event of multiple matched candidate molecules; and

(e) calculating a relative error and standard deviation thereof between the calibrated mass values and the theoretical mass in (d);

(f) determining a tolerance of the matching step using said standard deviation; and optionally

(g) repeating steps (b) – (f).

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5. (New) The biopolymer automatic identifying method according to claim 4, wherein said calibrating step comprises: (A) calculating a relative error between said mass values and the theoretical mass in (d); (B) estimating a systemic error of said mass values by creating a least square line by plotting the theoretical mass in (d) against said relative error; and (C) subtracting said systemic error from said mass values.

6. (New) The biopolymer automatic identifying method according to claim 4, wherein said sample comprises more than one biopolymer.

7. (New) The biopolymer automatic identifying method according to claim 4, wherein steps (b) – (f) are performed more than once.

8. (New) The biopolymer automatic identifying method according to claim 4, wherein each mass value is matched with one candidate molecule.